

**RAW SEQUENCE LISTING  
ERROR REPORT**

**BEST AVAILABLE**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/877,819A  
Source: OIP  
Date Processed by STIC: 5/9/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

01PE

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/877,819A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ✓ Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



**Does Not Comply**  
**Corrected Diskette Needed**

OIPE

## RAW SEQUENCE LISTING

DATE: 05/09/2002

PATENT APPLICATION: US/09/877,819A

TIME: 13:06:14

Input Set : A:\White.ST25.txt

Output Set: N:\CRF3\05092002\I877819A.raw

3 <110> APPLICANT: White, Scott  
 4 Torney, David  
 6 <120> TITLE OF INVENTION: Address/Capture Tags For Flow-Cytometry Based Minisequencing  
 8 <130> FILE REFERENCE: S-94,664  
 10 <140> CURRENT APPLICATION NUMBER: US 09/877,819A  
 11 <141> CURRENT FILING DATE: 2001-06-07  
 13 <160> NUMBER OF SEQ ID NOS: 55  
 15 <170> SOFTWARE: PatentIn version 3.0  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 20  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: none  
 22 <400> SEQUENCE: 1  
 23 tgaacccggg tatctcacca 20  
 26 <210> SEQ ID NO: 2  
 27 <211> LENGTH: 20  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: none  
 31 <400> SEQUENCE: 2  
 32 tggtagagata cccgggttca 20  
 35 <210> SEQ ID NO: 3  
 36 <211> LENGTH: 20  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: none  
 40 <400> SEQUENCE: 3  
 41 ggctttggag cgctctttaa 20  
 44 <210> SEQ ID NO: 4  
 45 <211> LENGTH: 20  
 46 <212> TYPE: DNA  
 47 <213> ORGANISM: none  
 49 <400> SEQUENCE: 4  
 50 ttaaagagcg ctccaaagcc 20  
 53 <210> SEQ ID NO: 5  
 54 <211> LENGTH: 20  
 55 <212> TYPE: DNA  
 56 <213> ORGANISM: none  
 58 <400> SEQUENCE: 5  
 59 aggaaaggag aggcgtcgtc 20  
 62 <210> SEQ ID NO: 6  
 63 <211> LENGTH: 20  
 64 <212> TYPE: DNA  
 65 <213> ORGANISM: none  
 67 <400> SEQUENCE: 6

invalid response, see error summary sheet, item 10

↓  
 The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

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Input Set : A:\White.ST25.txt

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68 gacgacgcct ctcctttcct                                20
71 <210> SEQ ID NO: 7
72 <211> LENGTH: 20
73 <212> TYPE: DNA
74 <213> ORGANISM: none
76 <400> SEQUENCE: 7
77 aaccacctta agggacggac                                20
80 <210> SEQ ID NO: 8
81 <211> LENGTH: 20
82 <212> TYPE: DNA
83 <213> ORGANISM: none
85 <400> SEQUENCE: 8
86 gtccgtccct taaggtgggt                                20
89 <210> SEQ ID NO: 9
90 <211> LENGTH: 20
91 <212> TYPE: DNA
92 <213> ORGANISM: none
94 <400> SEQUENCE: 9
95 gtaccctcgg aaggacccaa                                20
98 <210> SEQ ID NO: 10
99 <211> LENGTH: 20
100 <212> TYPE: DNA
101 <213> ORGANISM: none
103 <400> SEQUENCE: 10
104 ttgggtcctt ccgagggtag                                20
107 <210> SEQ ID NO: 11
108 <211> LENGTH: 20
109 <212> TYPE: DNA
110 <213> ORGANISM: none
112 <400> SEQUENCE: 11
113 aaagtcgcgc ccagaacctc                                20
116 <210> SEQ ID NO: 12
117 <211> LENGTH: 20
118 <212> TYPE: DNA
119 <213> ORGANISM: none
121 <400> SEQUENCE: 12
122 gaggttctgg gcgcgacttt                                20
125 <210> SEQ ID NO: 13
126 <211> LENGTH: 20
127 <212> TYPE: DNA
128 <213> ORGANISM: none
130 <400> SEQUENCE: 13
131 tgtgttcggc gacttggtag                                20
134 <210> SEQ ID NO: 14
135 <211> LENGTH: 20
136 <212> TYPE: DNA
137 <213> ORGANISM: none
139 <400> SEQUENCE: 14
140 ctaccaagtc gccgaacaca                                20

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Input Set : A:\White.ST25.txt

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143 <210> SEQ ID NO: 15
144 <211> LENGTH: 20
145 <212> TYPE: DNA
146 <213> ORGANISM: none
148 <400> SEQUENCE: 15
149 acctgctggg ccgggatggtt                20
152 <210> SEQ ID NO: 16
153 <211> LENGTH: 20
154 <212> TYPE: DNA
155 <213> ORGANISM: none
157 <400> SEQUENCE: 16
158 aacatcccgg cccagcaggt                20
161 <210> SEQ ID NO: 17
162 <211> LENGTH: 20
163 <212> TYPE: DNA
164 <213> ORGANISM: none
166 <400> SEQUENCE: 17
167 tttcaggttc cacggcattg                20
170 <210> SEQ ID NO: 18
171 <211> LENGTH: 20
172 <212> TYPE: DNA
173 <213> ORGANISM: none
175 <400> SEQUENCE: 18
176 caatgccgtg gaacctgaaa                20
179 <210> SEQ ID NO: 19
180 <211> LENGTH: 20
181 <212> TYPE: DNA
182 <213> ORGANISM: none
184 <400> SEQUENCE: 19
185 aaatggcctt gctgtctacg                20
188 <210> SEQ ID NO: 20
189 <211> LENGTH: 20
190 <212> TYPE: DNA
191 <213> ORGANISM: none
193 <400> SEQUENCE: 20
194 cgtagacagc aaggccattt                20
197 <210> SEQ ID NO: 21
198 <211> LENGTH: 20
199 <212> TYPE: DNA
200 <213> ORGANISM: none
202 <400> SEQUENCE: 21
203 gttccggttt cgccatgaga                20
206 <210> SEQ ID NO: 22
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: none
211 <400> SEQUENCE: 22
212 tctcatggcg aaaccggaac                20
215 <210> SEQ ID NO: 23

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Input Set : A:\White.ST25.txt

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```

216 <211> LENGTH: 20
217 <212> TYPE: DNA
218 <213> ORGANISM: none
220 <400> SEQUENCE: 23
221 acgtgtttcc cgccaaatat 20
224 <210> SEQ ID NO: 24
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: none
229 <400> SEQUENCE: 24
230 atatttggcg ggaaacacgt 20
233 <210> SEQ ID NO: 25
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: none
238 <400> SEQUENCE: 25
239 ggctgctaaa ggcgttctaa 20
242 <210> SEQ ID NO: 26
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: none
247 <400> SEQUENCE: 26
248 ttagaacgcc ttagcagcc 20
251 <210> SEQ ID NO: 27
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: none
256 <400> SEQUENCE: 27
257 attaggggtgc gcgccatctt 20
260 <210> SEQ ID NO: 28
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: none
265 <400> SEQUENCE: 28
266 aagatggcgc gcaccctaata 20
269 <210> SEQ ID NO: 29
270 <211> LENGTH: 20
271 <212> TYPE: DNA
272 <213> ORGANISM: none
274 <400> SEQUENCE: 29
275 cgaagcattt ggccaattta 20
278 <210> SEQ ID NO: 30
279 <211> LENGTH: 20
280 <212> TYPE: DNA
281 <213> ORGANISM: none
283 <400> SEQUENCE: 30
284 taaattggcc aaatgcttcg 20
287 <210> SEQ ID NO: 31
288 <211> LENGTH: 20

```

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PATENT APPLICATION: US/09/877,819A

TIME: 13:06:14

Input Set : A:\White.ST25.txt

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```

289 <212> TYPE: DNA
290 <213> ORGANISM: none
292 <400> SEQUENCE: 31
293 cagttcgccc aaaggatagg                                20
296 <210> SEQ ID NO: 32
297 <211> LENGTH: 20
298 <212> TYPE: DNA
299 <213> ORGANISM: none
301 <400> SEQUENCE: 32
302 cctatccttt gggcgaactg                                20
305 <210> SEQ ID NO: 33
306 <211> LENGTH: 20
307 <212> TYPE: DNA
308 <213> ORGANISM: none
310 <400> SEQUENCE: 33
311 gacgacgcct ctcctttcct                                20
314 <210> SEQ ID NO: 34
315 <211> LENGTH: 23
316 <212> TYPE: DNA
317 <213> ORGANISM: none
319 <400> SEQUENCE: 34
320 cggaccatgt gtcaacttat gcc                            23
323 <210> SEQ ID NO: 35
324 <211> LENGTH: 20
325 <212> TYPE: DNA
326 <213> ORGANISM: none
328 <400> SEQUENCE: 35
329 aggaaaggag aggcgtcgtc                                20
332 <210> SEQ ID NO: 36
333 <211> LENGTH: 20
334 <212> TYPE: DNA
335 <213> ORGANISM: none
337 <400> SEQUENCE: 36
338 ttaaagagcg ctccaaagcc                                20
341 <210> SEQ ID NO: 37
342 <211> LENGTH: 26
343 <212> TYPE: DNA
344 <213> ORGANISM: none
346 <400> SEQUENCE: 37
347 tcaacttatg ccgcgtttgt acagac                        26
350 <210> SEQ ID NO: 38
351 <211> LENGTH: 20
352 <212> TYPE: DNA
353 <213> ORGANISM: none
355 <400> SEQUENCE: 38
356 ggctttggag cgctctttaa                                20
359 <210> SEQ ID NO: 39
360 <211> LENGTH: 20
361 <212> TYPE: DNA

```

VERIFICATION SUMMARY

DATE: 05/09/2002

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TIME: 13:06:15

Input Set : A:\White.ST25.txt

Output Set: N:\CRF3\05092002\I877819A.raw